AMENDMENTS TO THE CLAIMS:

Amend the claims as follows:

Claims 1-23. (Canceled)

24. (Currently Amended) An isolated polynucleic acid sequence consisting of 8 or more contiguous nucleotides selected from the region spanning positions 1 to 346 of the Core region of an HCV subtype 3c genomic sequence, wherein said polynucleic acid sequence is capable of hybridizing to HCV type 3c, but not another type or subtype of HCV; or

the complement of said polynucleic acid, wherein said polynucleic acid contains at least one genotype 3c-specific nucleotide.

25. (Currently Amended) An isolated Hepatitis C virus polynucleic acid selected from the group consisting of:

(i) the nucleotide sequence of SEQ ID NO:147,

(ii) at least 8 contiguous nucleotides of a nucleotide sequence having at least one genotype-specific nucleotide from the region spanning positions 1 to 346 of the ~~957 of the~~ Core ~~or Core/E1~~ region of HCV subtype 3c, and,

(iii) the complement of the nucleotide sequence of (i) or (ii).

26. (Previously Presented) A recombinant vector comprising a vector sequence and a prokaryotic, eukaryotic or viral promotor sequence operably linked to a

polynucleic acid sequence of claim 24.

27. (Previously Presented) A recombinant vector comprising a vector sequence and a prokaryotic, eukaryotic or viral promotor sequence operably linked to a polynucleic acid sequence of claim 25.

28. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

(i) providing a sample nucleic acid,

(ii) determining the presence of a polynucleic acid sequence according to claim 24, by means of a sequencing reaction, and,

(iii) inferring from the presence of one or more of these HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

29. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

(i) providing a sample nucleic acid,

(ii) determining the presence of a polynucleic acid sequence according to claim 25, by means of a sequencing reaction, and,

(iii) inferring from the presence of one or more of these HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

30. (Previously Presented) A method of detecting or screening for one or more

HCV genotypes present in a biological sample, comprising the following steps:

(i) providing a sample nucleic acid,

(ii) specifically amplifying a polynucleic acid sequence according to claim 24, and,

(iii) inferring from the presence of one or more amplified HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

31. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

(i) providing a sample nucleic acid,

(ii) specifically amplifying a polynucleic acid sequence according to claim 25, and,

(iii) inferring from the presence of one or more amplified HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

32. (Previously Presented) An isolated HCV polynucleic acid according to claim 24, wherein said polynucleic acid is capable of acting as a primer for HCV type- or subtype-specific amplification, and wherein said polynucleic acid consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.

33. (Previously Presented) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a primer for HCV type- or

subtype-specific amplification, and wherein said polynucleic acid consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.

34. (Previously Presented) An isolated HCV polynucleic acid according to claim 24, wherein said polynucleic acid is capable of acting as a primer of a HCV subtype 3c nucleic acid sequence, and wherein said polynucleic acid consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.

35. (Previously Presented) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a primer of a HCV subtype 3c nucleic acid sequence, and wherein said polynucleic acid consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.

36. (Previously Presented) An isolated HCV polynucleic acid according to claim 24, wherein said polynucleic acid is capable of acting as a probe for specific hybridization to a HCV type or subtype-specific, and wherein said polynucleic acid consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.

37. (Previously Presented) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a probe for specific hybridization to a HCV type or subtype-specific, and wherein said polynucleic acid

consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.

38. (Previously Presented) An isolated HCV polynucleic acid according to claim 24, wherein said polynucleic acid is capable of acting as a probe for specific hybridization to a HCV subtype 3c nucleic acid sequence, and wherein said polynucleic acid consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.

39. (Previously Presented) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a probe for specific hybridization to a HCV subtype 3c nucleic acid sequence, and wherein said polynucleic acid consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.

40. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a polynucleic acid sequence according to claim 24.

41. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a polynucleic acid sequence according to claim 25.

42. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a primer according to claim 32.

43. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a primer according to claim 33.

44. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a primer according to claim 34.

45. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a primer according to claim 35.

46. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a probe according to claim 36.

47. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a probe according to claim 37.

48. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a probe according to claim 38.

49. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a probe according to claim 39.

50. (Previously Presented) A method for determining the presence of HCV

genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) amplifying the nucleic acid with at least one primer according to claim 32,

(iii) detecting the amplified nucleic acids,

(iv) inferring the presence of one or more genotypes of HCV present from the observed pattern of amplified fragments.

51. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) amplifying the nucleic acid with at least one primer according to claim 33,

(iii) detecting the amplified nucleic acids,

(iv) inferring the presence of one or more genotypes of HCV present from the observed pattern of amplified fragments.

52. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) amplifying the nucleic acid with at least one primer according to claim 34,

(iii) detecting the amplified nucleic acids,

(iv) inferring the presence of one or more genotypes of HCV present from the observed pattern of amplified fragments.

53. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) amplifying the nucleic acid with at least one primer according to claim 35,

(iii) detecting the amplified nucleic acids,

(iv) inferring the presence of one or more genotypes of HCV present from the observed pattern of amplified fragments.

54. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) optionally amplifying the nucleic acid with at least one primer,

(iii) hybridizing the nucleic acids of the biological sample with one or more probes according to claim 36, with said probes being optionally attached to a solid substrate,

(iv) optionally washing,

(v) detecting the hybrids formed,

(vi) inferring the presence of one or more genotypes of HCV present from the observed hybridization pattern.

55. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) optionally amplifying the nucleic acid with at least one primer,

(iii) hybridizing the nucleic acids of the biological sample with one or more probes according to claim 37, with said probes being optionally attached to a solid substrate,

(iv) optionally washing,

(v) detecting the hybrids formed,

(vi) inferring the presence of one or more genotypes of HCV present from the observed hybridization pattern.

56. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) optionally amplifying the nucleic acid with at least one primer,

(iii) hybridizing the nucleic acids of the biological sample with one or more probes according to claim 38, with said probes being optionally attached to a solid substrate,

(iv) optionally washing,

(v) detecting the hybrids formed,

(vi) inferring the presence of one or more genotypes of HCV present from the observed hybridization pattern.

57. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) optionally amplifying the nucleic acid with at least one primer,

(iii) hybridizing the nucleic acids of the biological sample with one or more probes according to claim 39, with said probes being optionally attached to a solid substrate,

(iv) optionally washing,

(v) detecting the hybrids formed,

(vi) inferring the presence of one or more genotypes of HCV present from the observed hybridization pattern.